

1/21

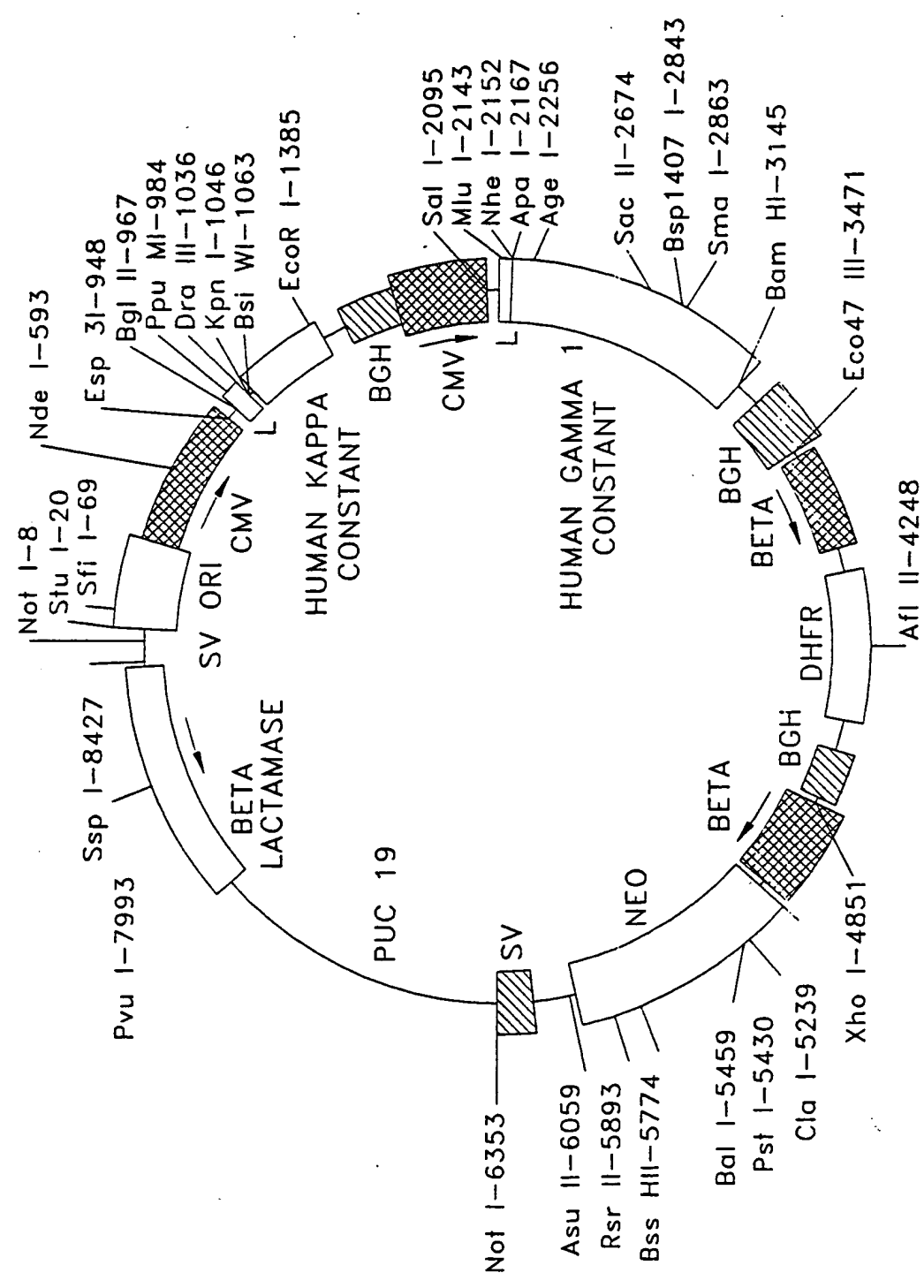


FIG. 1

2/21

LINKER #1 15bp | SV40 ORIGIN=332bp
 GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
 AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
 GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTGTCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
 GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAAT TAATTCCCCT 360
 AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
 GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTTG 480
 CMV PROMOTER-ENHANCER=567bp
 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
 TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
 AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC CCTGGCATTG TGCCAGTAC 660
 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
 ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
 Bgl II | LEADER=60bp
 CATCACAGAT CTCTACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG 1020
 CTCCCAGGTG CACGATGTGA +1 | 101 102 | 107 108
 TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
 1038 9 | 1062 3 Bsi WI
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1140
 TGCTGTCTGA ATAATTCTA TCCAGAGAG GCCAAAGTAC AGTGGAAAGT GGATAACGCC 1200
 HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
 TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1380
 STOP
 LIGHT
 CHAIN | Eco RI | LINKER #4=85bp
 TGTTCGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1440
 1386 7 | 1471 2
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500

FIG. 2A

3/21

GTTTGCCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCTTTTCC 1560
 TAATAAAATG AGGAAATTGC **BGH poly A=231bp** ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680
 GCGGTGGGCT CTATGGAACC **LINKER #5=15bp** AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740
 1702 3 1717 8
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860
 GGCAGTACAT CAATGGGCGT **CMV PROMOTER-ENHANCER=334bp** GGATAGCGGT TTGACTCACG GGGATTTCAC AGTCTCCACC 1920
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAATGTC 1980
 GTAACAATC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
 TAAGCAGAGC **LINKER #6=7bp** TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG **Sal I** ACCCGTCGAC 2100
 2051 2 2058 9
 ATGGGTTGGA GCCTCATCTT **LEADER=51bp** GCTCTTCCTT GTCGCTGTTG **Mlu I 2151 2 Nhe I** CTACGCGTGT CGCTAGCACC 2160
START HEAVY CHAIN -5 -4 -3 114 115
 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220
 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA 2280
 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
 TCCCTCAGCA GCGTGGTGAC **HUMAN GAMMA 1 CONSTANT** CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 2580
 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGA CTACAAG 2760
 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAGG 2880
 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

4/21

GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
 STOP HEAVY CHAIN | Bam HI LINKER #7=81bp
 CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180
 3144 5
 TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC CTCGACTGTG CTTTCTAGTT 3240
 3225 6
 GCCAGCCATC TGTTGTTTGC CCTTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC 3300
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360
 CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA 3420
 LINKER #8=34bp
 GGCATGCTGG GGATGCGGTG GGCTCTATGG AACCAGCTGG GGCTCGACAG CGCTGGATCT 3480
 3456 7
 CCCGATCCCC AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 3540
 3490 1
 AATTTTAAAC CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATFTGCTT 3840
 LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp
 CTGACATAGT TGTGTTGGGA GCTTGGATAG CTTGGACAGC TCAGGGCTGC GATTTGCGGC 3900
 3856 7 3875 6
 CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGGTAGGATT TTATCCCCGC TGCCATCAT 3960
 3957 8
 GTTCGACCAT TGAAGTGCAT CGTCGCCGTG TCCCAAATA TGGGGATTGG CAAGAACGGA 4020
 GACCTACCCT GGCCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080
 TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTATGGGTA GGAAAACCTG GTTCTCCATT 4140
 MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON
 CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAAA 4200
 GAACCAACCAC GAGGAGCTCA TTTTCTTGCC AAAAGTTTGG ATGATGCCTT AAGACTTATT 4260
 GAACAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTTGGG TAGTCGGAGG CAGTTCTGTT 4320
 TACCAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
 GAATTTGAAA GTGACACGTT TTTCCAGAA ATTGATTTGG GGAAATATAA ACTTCTCCCA 4440
 GAATACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAG GCATCAAGTA TAAGTTTGAA 4500

FIG. 2C

5/21

STOP DHFR
 GTCTACGAGA AGAAAGAC TA ACAGGAAGAT GCTTTCAAGT TCTCTGCTCC CCTCCTAAAG 4560
 4521 2
 3' UNTRANSLATED DHFR=82bp LINKER #10=10bp
 TCATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGCC 4620
 4603 4 4613 4
 TTCTAGTTGC CAGCCATCTG TTGTTTGCCC CTCCCCCGTG CCTTCCTTGA CCCTGGAAGG 4680
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 TGCCACTCCC ACTGTCCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740
 GTGTCATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA CCAGCTGGGG CTCGAGCTAC 4860
 4844 5 LINKER #11=17bp
 TAGCTTTGCT TCTCAATTC TTATTTGCAT AATGAGAAAA AAAGGAAAAT TAATTTTAAC 4920
 ACCAATTCAG TAGTTGATTG AGCAAATGCG TTGCCAAAAA GGATGCTTTA GAGACAGTGT 4980
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040
 GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATTC 5100
 CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160
 AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTTGCT TCTGACATAG 5220
 TTGTGTTGGG LINKER #12=21bp START NEO
 5227 8 AGCTTGGATC GATCCTCTAT GTTGAACAA GATGGATTGC ACGCAGGTTC 5280
 5248 9
 TCCGGCCGCT TGGGTGGAGA GGCTATTCGG CTATGACTGG GCACAACAGA CAATCGGCTG 5340
 CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGCGC CCGGTTCTTT TTGTCAAGAC 5400
 NEOMYCIN PHOSPHOTRANSFERASE
 CGACCTGTCC GGTGCCCTGA ATGAAGTGA GGACGAGGCA GCGCGGCTAT CGTGGCTGGC 5460
 795bp=264 AMINO ACIDS & STOP CODON
 CACGACGGGC GTTCCTTGCG CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520
 GCTGCTATTG GGCGAAGTGC CGGGGCAGGA TCTCCTGTCA TCTCACCTTG CTCCTGCCGA 5580
 GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640
 CCCATTCGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGAAGCCGG 5700
 TCTTGTGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760
 CGCCAGGCTC AAGGCGCGCA TGCCCGACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820
 CTGCTTGCCG AATATCATGG TGGAAAATGG CCGCTTTTCT GGATTCATCG ACTGTGGCCG 5880
 GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940
 GCTTGGCGGC GAATGGGCTG ACCGCTTCCT CGTGCTTTAC GGTATCGCCG CTTCCCGATTG 6000

FIG. 2D

FIG. 2E

7/21

GAAGTTTTAA ATCAATCTAA AGTATATATG **STOP BETA LACTAMASE** TACCAATGCT 7560
 TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTTCG TTCATCCATA GTTGCCCTGAC 7620
 TCCCCGTCGT GTAGATAACT ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680
 TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTTATC AGCAATAAAC CAGCCAGCCG 7740
 GAAGGGCCGA GCGCAGAAGT **BETA LACTAMASE=861bp** GGTCCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT 7800
 GTTGCCGGGA AGCTAGAGTA **286 AMINO ACID & STOP CODON** TTTGCGCAAC GTTGTTGCCA 7860
 TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC AGCTCCGGTT 7920
 CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAGCG GTTAGCTCCT 7980
 TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG 8040
 CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG 8100
 AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG 8160
 CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220
 AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTGATGT 8280
 AACCCACTCG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTCACCAGC GTTTCTGGGT 8340
 GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400
 GAATACT CAT **START BETA LACTAMASE** ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
 TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT 8520
 TTCCCCGAAA AGTGCCACCT

FIG. 2F

8/21

LINKER #1=15bp
 GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
 AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
 SV40 ORIGIN=332bp
 GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
 LINKER #2=13bp
 GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT 347 8 360
 AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
 GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCATTG 480
 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
 CVM PROMOTER-ENHANCER=567bp
 TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
 AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCAGTAC 660
 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
 ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
 LINKER #3=7bp
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 927 8 934 5 960
 Bgl 2 START LIGHT CHAIN NATURAL LEADER=66bp
 CATCACAGAT CTCTCACTAT GGATTTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT 978 9 1020
 GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1044 5+1 1080
 GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTGAAGTGT AAGTTACATC 1140
 CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCT GGATTTATGC CACATCCAAC 1200
 LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID
 CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTA CTCTCTC 1260
 ACCATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320
 BsiWI
 AACCCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1362 3 1380
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1440
 TGCCTGCTGA ATAACCTCTA TCCAGAGAG GCCAAAGTAC AGTGGAAAGG GGATAACGCC 1500

FIG. 3A

9/21

HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
 TCGGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680
 STOP
 LIGHT
 CHAIN Eco RI LINKER #4=81bp
 TGTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC 1740
 1646 7
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
 1771 2
 GTTTGCCCTT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCTTTTCC 1860
 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040
 2002 3 2017 8
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160
 CMV PROMOTER-ENHANCER=334bp
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCAGG GGGATTTCCA AGTCTCCACC 2220
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 2280
 GTAACAACCTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTAIA 2340
 LINKER #6=7bp Sal I
 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400
 2351 2 2358 9
 START
 HEAVY CHAIN SYNTHETIC & NATURAL LEADER Mlu I 2457 8
 ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGCGTGT CCTGTCCCAG 2460
 2401 -5 -4 -3 -2 -1 +1
 GTACAACCTGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTCC 2520
 TGCAAGGCTT CTGGCTACAC ATTTACCACT TACAATATGC ACTGGGTAAA ACAGACACCT 2580
 HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID
 GGTCTGGGGCC TGGAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640
 CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
 TACGGCGGTG ACTGGTACTT CAATGTCTGG GGCGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
 Nhe I
 GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG 2880
 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGG GACGGTGTCTG 2940
 HUMAN GAMMA 1 CONSTANT=993bp
 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA 3000

FIG. 3B

10/21

330 AMINO ACID & STOP CODON

GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3060
TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
AAATCTTGTG ACAAACCTCA CACATGCCCA CCGTGCCCAG CACCTGAACT CCTGGGGGGA 3180
CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480
AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC CCGGGATGAG 3540
CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600
GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAAC AAGACCAC GCCTCCCGTG 3660
CTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720
CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA TGAGGATCCG TTAACGGTTA CCAACTACCT 3840

STOP HEAVY CHAIN Bam HI LINKER #7=81bp
3813 4

AGACTGGATT CGTGACAACA TGCGGCCGTG ATATCTACGT ATGATCAGCC TGACTGTGC 3900

3894 5

CTTCTAGTTG CCAGCCATCT GTTGTGTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAE 3960
GTGCCACTCC CACTGTCCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA 4020

BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp

GGTGTCAATC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080

LINKER #8=34bp

ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140

4125 6

GCTGGATCTC CCGATCCCCA GCTTTGCTTC TCAATTTCTT ATTTCGATAA TGAGAAAAAA 4200
AGGAAAATTA ATTTAACAC CAATTCAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260

MOUSE BETA GLOBIN MAJOR PROMOTER=366bp

ATGCTTTAGA GACAGTGGTC TCTGCACAGA TAAGGACAAA CATTATTCAG AGGGAGTACC 4320
CAGAGCTGAG ACTCCTAAGC CAGTGAGTGG CACAGCATTC TAGGGAGAAA TATGCTTGTC 4380
ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGAAG GGCCAATCTG CTCACACAGG 4440
ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500

FIG. 3C

11/21

CATTGCTTC TGACATAGTT LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp
 GTGTTGGGAG CTGGATAGC TTGGACAGCT CAGGGCTGCC 4560
 4525 6 4544 5
 ATTCGCGCC AAACCTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620
START DHFR
 GCCATCATGG TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680
 4626 7
 AAGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
 ACCACAACCT CTTCACTGGA AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800
DHFR=564bp=187 AMINO ACID & STOP CODON
 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
 GAACTCAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGG TGATGCCTTA 4920
 AGACTTATTG AACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980
 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
 ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCAGAAA TTGATTTGGG GAAATATAAA 5100
 CTTCTCCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160
STOP DHFR 3' UNTRANSLATED DHFR=82bp
 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220
 5140 1
 CTCCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA LINKER #10
 =10bp] GATCAGCCTC 5280
 5272 3
 GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTITGCCCC TCCCCCGTGC CTTCTTGAC 5340
BOVINE GROWTH HORMONE POLYADENYLATION=231bp
 CCTGGAAGGT GCCACTCCCA CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCATTG 5400
 TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
LINKER #11
 TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TCGGTGGGC TCTATGGAAC CAGCTGGGGC 5520
 5513 4
 =17bp] TCGAGCTACT AGCTTTGCTT CTCAATTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 5580
 5530 1
 AATTTTAAAC CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA CTAGGGAGAA ATATGCTTGT CATCACCAGG 5700
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCAGG 5760
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880
LINKER #12=21bp START NEO
 CTGACATAGT TGTGTTGGGA GCTTGGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
 5896 7 5917 8
 CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTGGC TATGACTGGG CACAACAGAC 6000

FIG. 3D

12/21

AATCGGCTGC TCTGATGCCG CCGTGTTCCG GCTGTCAGCG CAGGGGCGGC CGGTTCTTTT 6060
 NEOMYCIN PHOSPHOTRANSFERASE=795bp=264 AMINO ACID & STOP CODON
 TGTCAGACC GACCTGTCCG GTGCCCTGAA TGAAGTGCAG GACGAGGCAG CGCGGCTATC 6120
 GTGGCTGGCC ACGACGGGCG TTCCTTGCGC AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
 AAGGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTCAT CTCACCTTGC 6240
 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCCG CGGCTGCATA CGCTTGATCC 6300
 GGCTACCTGC CCATTGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
 GGAAGCCGGT CTTGTGCATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
 CGAACTGTTT GCCAGGCTCA AGGCGCGCAT GCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
 TGGCGATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTTCTG GATTCATCGA 6540
 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT 6600
 TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GTATCGCCGC 6660
 TCCCGATTCT CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCT GAGCGGGACT 6720
 CTGGGGTTCT AAATGACCGA CCAAGCGACG CCCAACCTGC CATCAGGAGA TTTCGATTCC 6780
 3' UNTRANSLATED NEO=173bp
 ACCGCCGCCT TCTATGAAAG GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840
 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCCC ACCCGAACTT GTTTATTGCA 6900
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTTT 6960
 SV40 EARLY POLYADENYLATION REGION=133bp
 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
 LINKER #13=19bp
 GCGGCCGCGA TCCCGTCTGAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
 7037 8 PUC 19
 ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCCT 7140
 GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 7200
 AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 7260
 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC 7320
 GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG 7380
 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAAG AACCGTAAAA 7440
 7461=BACTERIAL ORIGIN OF REPLICATION
 AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC 7500

FIG. 3E

13/21

GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC 7560
 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC 7740
 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAAACAAA 7980
 CCACCGCTGG TAGCGGTGGT TTTTTTGTTC GCAAGCAGCA GATTACGCGC AGAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT 8100
 CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA 8160
 ATTAAAAATG AAGTTTTTAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT 8220
BETA LACTAMASE
 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG 8280
 TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC 8400
 BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON
 AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG 8520
 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA 8580
 GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8540
 TTAGCTCCTT CGGTCTCTCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA 8700
 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG 8760
 TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT 8820
 CTTGCCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
 TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
 GGTGATGTA ACCCACTCGT GCACCCAACCT GATCTTCAGC ATCTTTTACT TTCACCAGCG 9000
 TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
 GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT

FIG. 3F

14/21

LEADER

FRAME 1 Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val
 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC
 987 996 1005 1014 1023

-20 -15 -10
 -5 FR1 10
 Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser
 ATA ATG TCC AGA GGA CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT
 1038 1047 1056 1065 1074 1083

20 23 24 CDR1 27 29 30 34
 Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His
 CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AGT TAC ATC CAC
 1095 1104 1113 1122 1131 1140

35 FR2 40 45 49 50 CDR2
 Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn
 TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC
 1152 1161 1170 1179 1188 1197

55 56 57 60 FR3 65 70
 Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
 CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT
 1209 1218 1227 1236 1245 1254

75 80 85 88 89 90
 Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 CTC ACC ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG
 1266 1275 1284 1293 1302 1311

CDR3 95 97 98 100 FR4 105 107
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA
 1323 1332 1341 1350 1359

FIG. 4

15/21

LEADER

-19	-15	-10	-5
FRAME 1 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val			
ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC			
2409	2418	2427	2436 2445
-1	+1	FR1	10
Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys (Ala) Gly Ala Ser			
CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG GCC TCA			
2460	2469	2478	2487 2496 2505
20	25	30	31 CDR1 35 36
Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp			
GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC AAT ATG CAC TGG			
2517	2526	2536	2544 2553 2562
40 FR2	45	49	50 52 52A 53 54
Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn			
GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA GCT ATT TAT CCC GGA AAT			
2574	2583	2592	2601 2610 2615
55 CDR2 60	65	66 FR3	70
Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys			
GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC AAG GCC ACA TTG ACT GCA GAC AAA			
2631	2640	2649	2658 2667 2676
75	80	82	82A 82B 82C 83 85
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val			
TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC			
2688	2697	2706	2715 2724 2733
90	94	95	CDR3 100 100A 100B 100C 100D 101 102 103
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly			
TAT TAC TGT GCA AGA TCG ACT TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC			
2745	2754	2763	2772 2781 2790
105 FR4	110	113	
Ala Gly Thr Thr Val Thr Val Ser Ala			
GCA GGG ACC ACG GTC ACC GTC TCT GCA			
2802	2811	2820	

FIG. 5

16/21

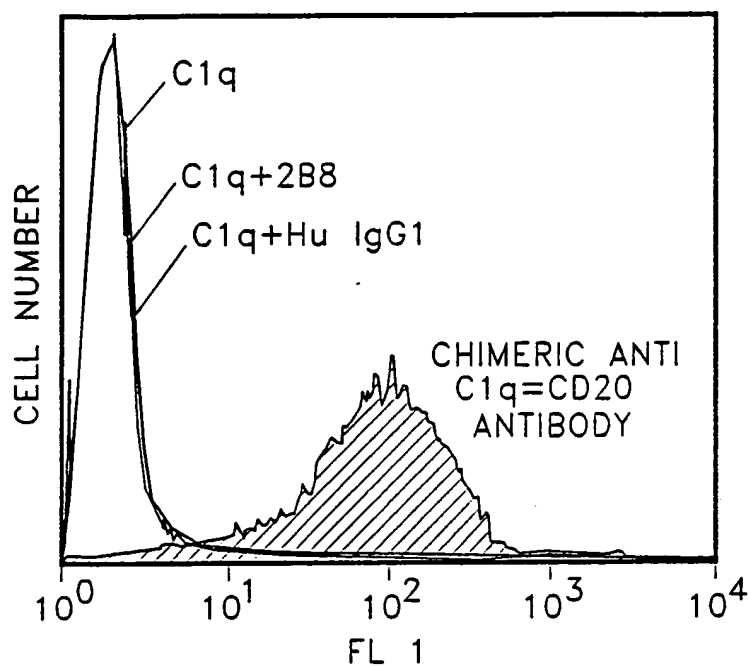


FIG. 6

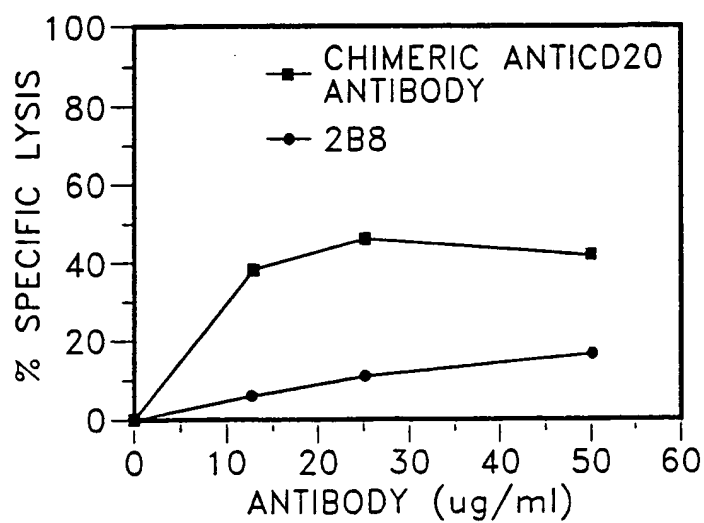
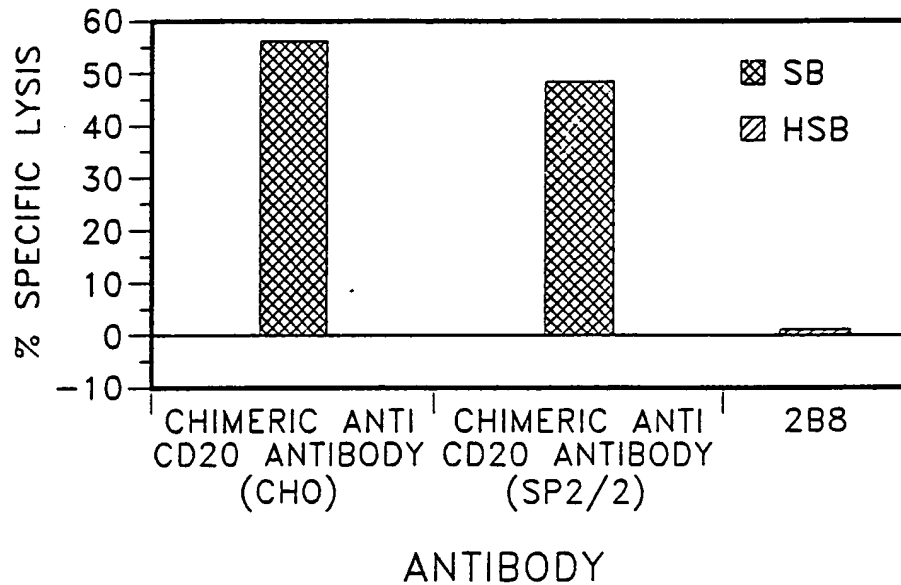
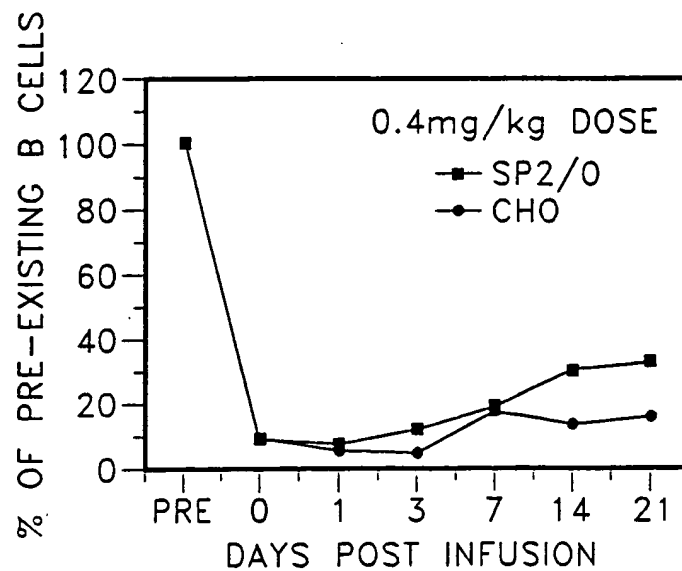
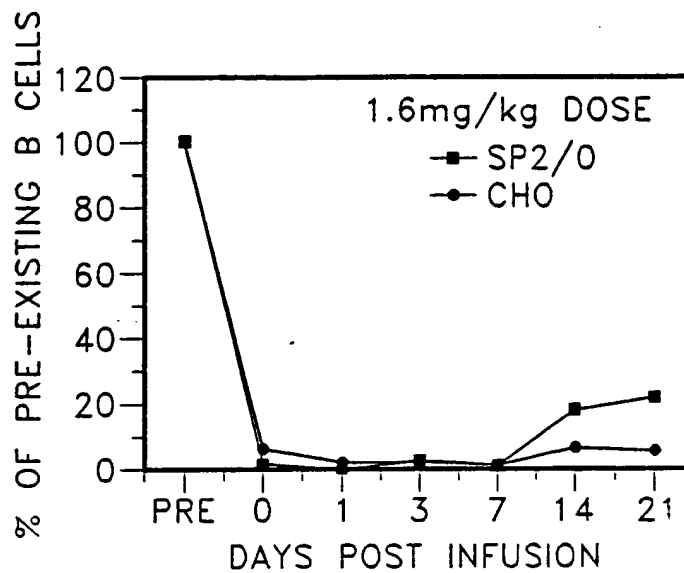
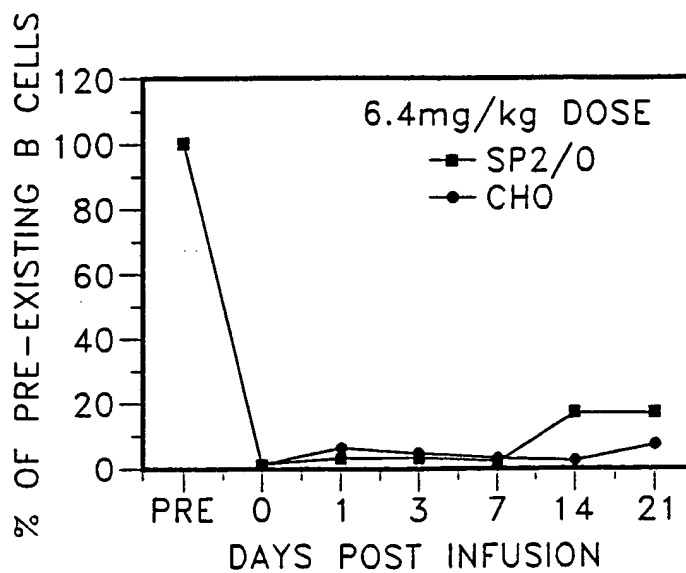


FIG. 7

17/21

*FIG. 8**FIG. 9A*

18/21

*FIG. 9B**FIG. 9C*

19/21

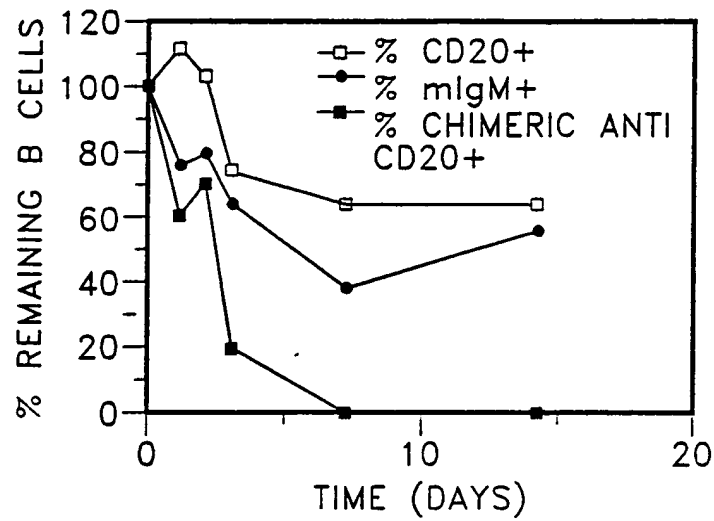


FIG. 10

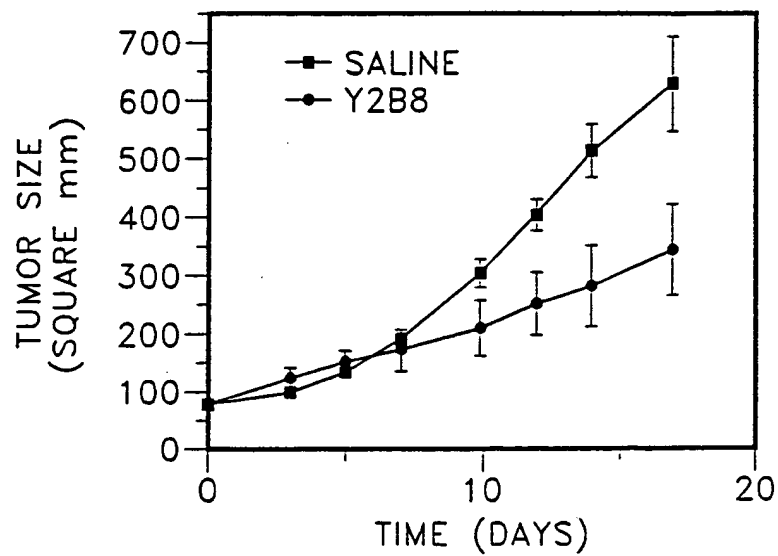


FIG. 11

20/21

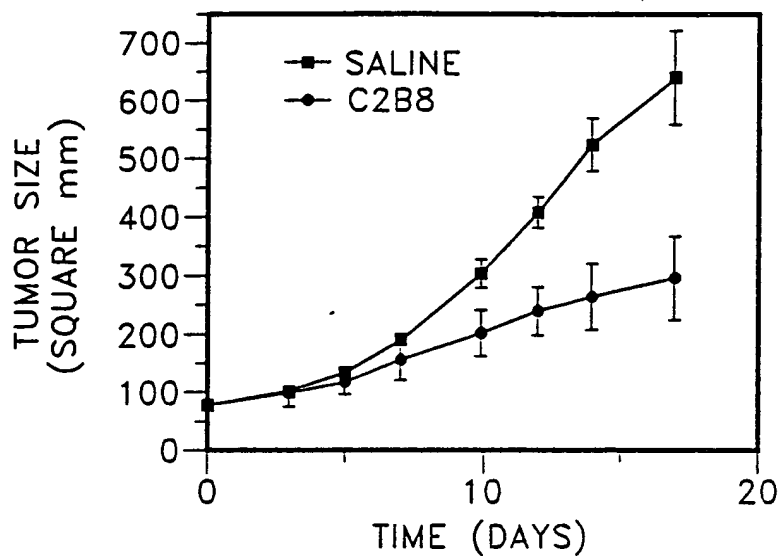


FIG. 12

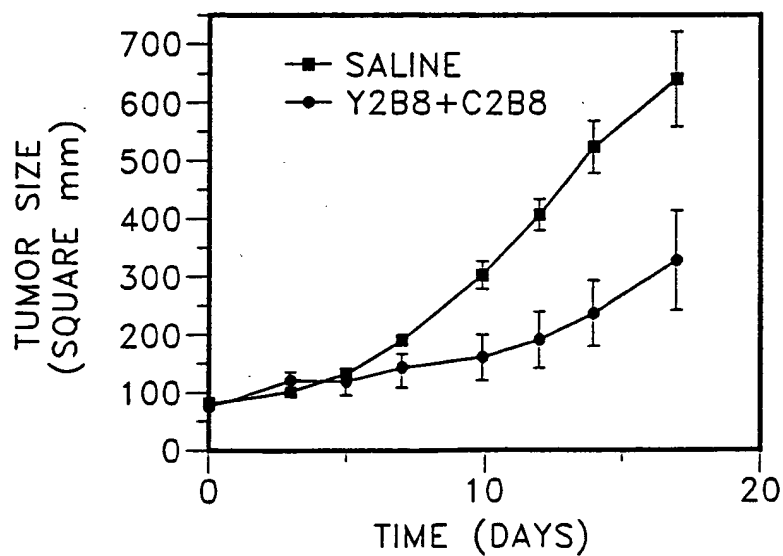
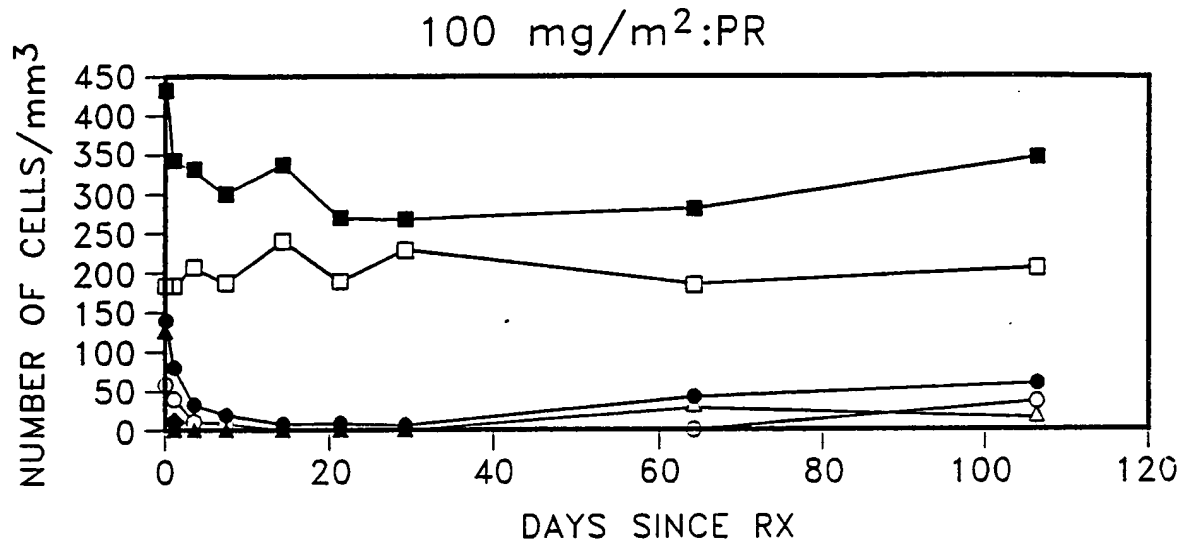


FIG. 13

21/21



(8/12/93)

FIG. 14A

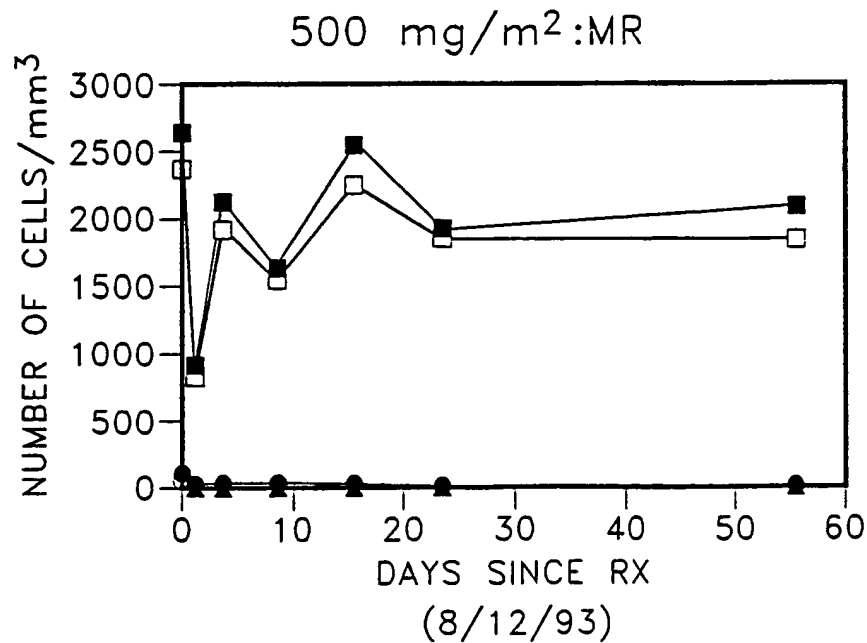


FIG. 14B

Figure 1
Binding of IDEC-C2B8 to CDW32 Mouse Fibroblast Cells Transfected with
Human Low Affinity Fc γ RII Membrane Receptors

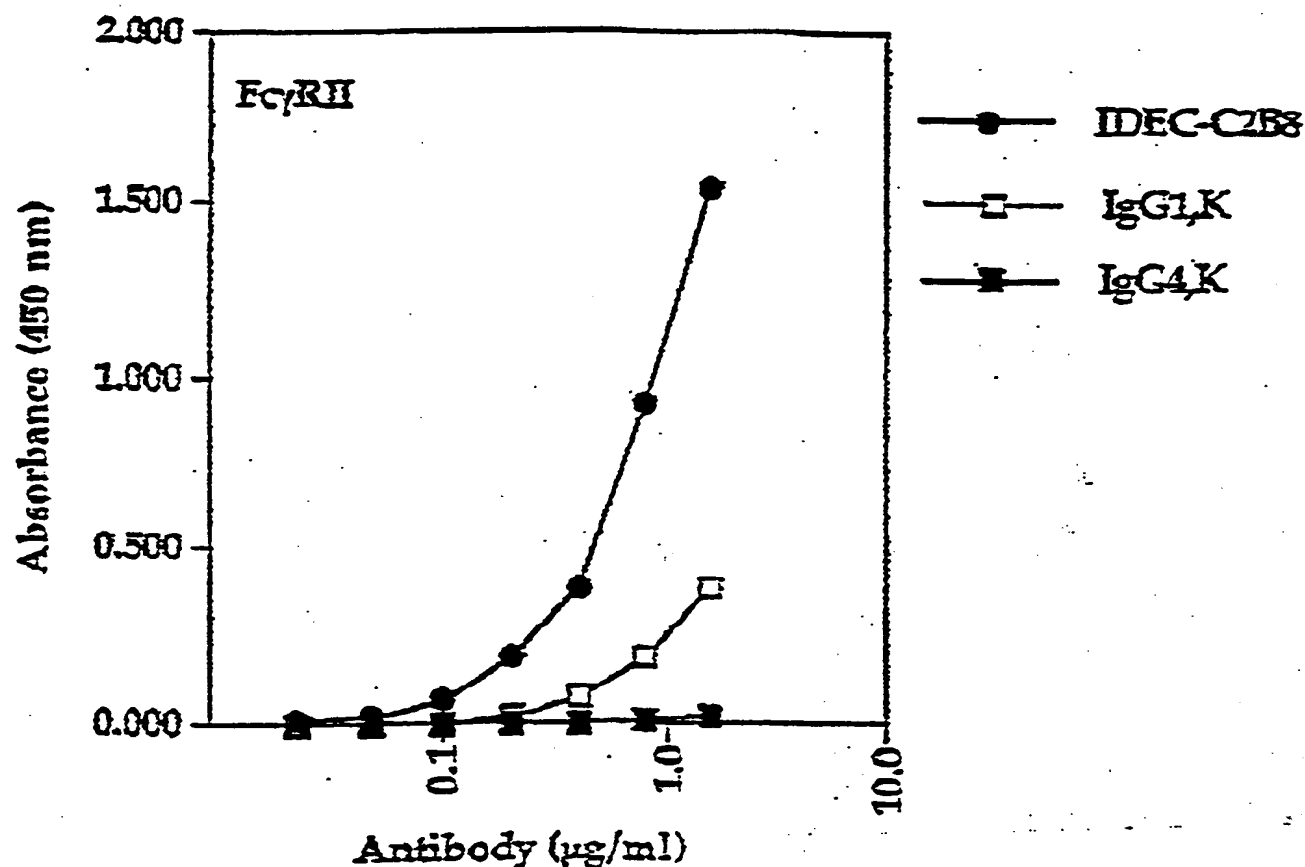


Figure 1. IDEC-C2B8 antibody was serially diluted in the absence of CD20, along with positive and negative isotype control human IgG1 and IgG4 antibodies. Aliquots were added in triplicate to sets of wells each containing Fc γ RII (human type II Fc receptor) transfected CDW32 mouse L cells. Binding of antibodies to Fc receptors was determined by ELISA. These results indicate that IDEC-C2B8 binds much more strongly to the low affinity human Fc γ RII receptor than typical human IgG1 antibodies with similar receptor binding sites.